

```

OM of: US-08-911-423-2 to: N_Geneseq_34 :* out_format : pfs
About: Results were produced by the GenCore software, version
Copyright (C) 1993-1998 Compugen Ltd.

Date: Aug 5, 1999 2:43 PM

Command line parameters:
-MODEL=frame+-p2n.model -DEV=xmlp
-0=/cgn_1/uspto_spool/US0891143/runat_05081999-084745-115
--DB=N_Geneseq_34 -OEMT=fasta -SUFFIX=rng -GAPOP=12_000
-GAPEXT4_0.000 -MINP=0.100 -LOOPCL=0.000 -XGAPEXT=0.000
-GAPAPOP_4_500 -QGAPEXT=0.050 -XGAPOP=10_000 -XGAPEXT=0.500
-FGAPOP_6_000 -FGAPEXT=7_000 -YGAPOP=10_000 -YGAPEXT=0.500
-DELOP_6_0000 -DELEX7_7_000 -START1=1-MATRIX=pam150
-TRANSFORM=_cdi -LIST=45 -DOCALIGN=2000 -THR SCORE=escore
-ALIGN=15 -MODE=LOCAL -OUTENT=pfs -NORM=stat USER=US089114
-NCPU=6 -ICPU=3 -WAIT -THREADS=1

Search information block:
Entry: US-08-911-423-2
Entry length: 228
Database: N_Geneseq_34 :*
Database sequences: 240522
Database length: 94065509
Search time (sec): 110.750000

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N_Geneseq_34:T36585	+	100..50	194..39	0..0024	1206	Osteoclastogenesis inhibitor
N_Geneseq_34:V20568	+	100..50	194..39	0..0024	1206	Human OCIF genome cDNA. Inh
N_Geneseq_34:T96063	+	100..50	193..14	0..0029	1355	Human osteoprotegerin cDNA.

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
-MODEL=frame+**p2n**.model -D

DT 29-SEP-1998 (first entry)
 DE Mouse glucocorticoid induced TNFR-family related protein cDNA.
 KW Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;
 GITR; tumour necrosis factor; apoptosis; hodgkin's disease; GITR-B;
 GITR-C; ds.

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-TRANS=nhuman10.cdi LIST5 -DOCALLIG=200 -THR SCORE=escore
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-NCPU=6 -ICPU=3 -WAIT -THREADS=1

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Search information block:
serv: US-08-911-423-2

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erly length: 228
Database: N_Geneseq_34:*
Database sequences: 240622
Database length: 94065609
Search time (sec): 110.570000
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score_list:							
Sequence	Zscore	Strd	Orig	Escore	Len	Documentation	
N_Genesed_34_V32773	+1195.00	2631.41	4.4e-139	1020	Mouse glucocorticoid induced T lymphocyte activity and cell death rescue, useful to, e.g. develop products to suppress lymphocyte activity and induce apoptosis	PT PT PT PT PS	Claim 1; Pages 34-36; 53PP; English.
N_Genesed_34_V19152	+1195.00	2610.87	4.7e-139	1073	Mouse glucocorticoid induced T lymphocyte activity and cell death rescue, useful to, e.g. develop products to suppress lymphocyte activity and induce apoptosis	PT PT PT PT PS	The present claimed sequence represents a mouse glucocorticoid induced TNFR-family related protein (GTR-B) cDNA isolated from a mouse T-cell cDNA library. The invention also claims for the GTR-B f (V32774) and GTR-C (V32775) cDNAs which are splicing variants of GTR cDNA. The GTRs are claimed to be useful for stimulating lymphocyte activity and cell death rescue. GTR antagonists are claimed to be useful for suppressing the lymphocyte activity and for inducing apoptosis. GTR cDNAs and the proteins they encode are also claimed to be useful for suppressing growth of tumour cells over-expressing GTR or for the treatment of refractory hodgkin's disease.
N_Genesed_34_V32774	+1195.00	2511.56	6.3e-135	1031	Mouse GTR-B cDNA. New isolate	CC	CC
N_Genesed_34_V32775	+1195.00	2511.73	4.4e-134	1007	Mouse GTR-C cDNA. New isolate	CC	CC
N_Genesed_34_V19153	+660.50	1442.32	2.5e-73	1006	Nucleotide sequence of the human truncated human 312C2 protein f	CC	CC
N_Genesed_34_V19154	+509.50	1109.90	2.5e-54	723	H4-1BB receptor protein cDNA. N	CC	CC
N_Genesed_34_Q86126	+176.00	356.29	6.5e-13	1415	Human 4-1BB polypeptide coding	CC	CC
N_Genesed_34_Q75424	+176.00	360.66	1.3e-12	1415	Human 4-1BB receptor cDNA clone	CC	CC
N_Genesed_34_T91026	+176.00	360.66	1.3e-12	1415	DNA encoding a human 4-1BBSV 1	CC	CC
N_Genesed_34_T91027	+174.00	360.53	1.4e-12	946	Human receptor H4-1BB cDNA. Mon	CC	CC
N_Genesed_34_T91028	+157.00	324.01	1.5e-10	838	Human receptor induced by lymph	CC	CC
N_Genesed_34_Q92086	+158.00	320.43	2.3e-10	1439	Human 4-1BB polypeptide coding	CC	CC
N_Genesed_34_Q75428	+153.50	317.05	3.5e-10	768	Mouse 4-1BB receptor cDNA clone	CC	CC
N_Genesed_34_T91027	+153.50	317.16	3.5e-10	768	Mouse receptor 4-1BB CDNA. Mon	CC	CC
N_Genesed_34_T91028	+153.50	305.16	1.6e-09	2347	Mouse receptor 4-1BB CDNA. Mon	CC	CC
N_Genesed_34_T91028	+153.50	305.15	1.6e-09	2350	4-1BB receptor protein cDNA. N	CC	CC
N_Genesed_34_T00826	+113.50	303.50	1.7e-09	618	Mouse type-II membrane polypept	CC	CC
N_Genesed_34_V32640	+113.50	230.50	2.4e-05	618	Mouse OX40 extracellular domain	CC	CC
N_Genesed_34_V32639	+117.00	230.16	2.4e-05	1317	Plasmid pDC406/OX40Fc* encodi	CC	CC
N_Genesed_34_V32636	+117.00	230.16	2.5e-05	1317	OX40/Fc cDNA. Purified polype	CC	CC
N_Genesed_34_V41379	+115.50	223.01	6.2e-05	1878	Murine NF-kB receptor activato	CC	CC
N_Genesed_34_V41373	+115.50	223.01	6.2e-05	1878	Murine NF-kB receptor activato	CC	CC
N_Genesed_34_V41375	+109.00	211.77	0.0003	1391	RANK partial polypeptide encod	CC	CC
N_Genesed_34_V41369	+109.00	211.77	0.0003	1391	RANK partial polypeptide encod	CC	CC
N_Genesed_34_Q88758	+105.00	198.55	0.0006	1057	ACT-4 h-1 surface receptor cl	CC	CC
N_Genesed_34_T040458	+105.00	205.82	0.0006	1057	ACT-4 h-1 receptor cDNA sequen	CC	CC
N_Genesed_34_V41376	+109.00	203.04	0.0008	3136	NF-kB receptor activator RANK	CC	CC
N_Genesed_34_V41370	+109.00	203.04	0.0008	3136	NF-kB receptor activator RANK	CC	CC
N_Genesed_34_Q93257	+101.00	199.47	0.0013	834	Human OX-40 cDNA. Nucleic acid	CC	CC
N_Genesed_34_T33166	+102.00	198.88	0.0014	1083	Mutated OCIF, OCIF-DCR1, codin	CC	CC
N_Genesed_34_V33174	+100.50	198.55	0.0014	819	Mutated OCIF, OCIF-CD2, coding	CC	CC
N_Genesed_34_V62467	+100.00	197.66	0.0016	2781	Human dendritic cell receptor	CC	CC
N_Genesed_34_T33179	+100.50	196.78	0.0016	966	Mutated OCIF, OCIF-CSph, coding	CC	CC
N_Genesed_34_T33171	+100.50	196.58	0.0018	984	Mutated OCIF, OCIF-DD2, coding	CC	CC
N_Genesed_34_T33173	+100.50	195.82	0.0020	1056	Mutated OCIF, OCIF-CC, coding	CC	CC
N_Genesed_34_T35475	+100.50	194.69	0.0023	1173	Human tumour necrosis factor 1	CC	CC
N_Genesed_34_T33178	+100.50	194.61	0.0024	1182	Mutated OCIF, OCIF-CBst, codin	CC	CC
N_Genesed_34_V24487	+100.50	194.55	0.0024	1188	Modified TRI receptor coding s	CC	CC
N_Genesed_34_T33172	+100.50	194.45	0.0024	1200	Mutated OCIF, OCIF-Cl, coding	CC	CC
N_Genesed_34_T33163	+100.50	194.39	0.0024	1206	Mutated OCIF, OCIF-C21S, codin	CC	CC
N_Genesed_34_T33164	+100.50	194.39	0.0024	1206	Mutated OCIF, OCIF-C23S, codin	CC	CC
N_Genesed_34_T33165	+100.50	194.39	0.0024	1206	Mutated OCIF, OCIF-GAGCTGTATGCAGCTGTATGCC	CC	CC
N_Genesed_34_V41370	+100.50	194.39	0.0024	1206	GlycylGluaspCysProLysGluArgCysIleCysValThrProGluTy	CC	CC
N_Genesed_34_V41370	+100.50	194.39	0.0024	1206	alGlnAsnGlySerGlyAsnAsnThrArgCysCysSerLeuTyrAlaPro	CC	CC
N_Genesed_34_V41370	+100.50	194.39	0.0024	1206	ATGGGGCATGGCCATGGCTATGGCTCATGGTCTGTCGTCGCGGA	CC	CC
N_Genesed_34_V41370	+100.50	194.39	0.0024	1206	MetGlyAlaTPAlaLeuLeuTyrGlyValSerMetLeuCysValLeuAs	CC	CC
N_Genesed_34_V41370	+100.50	194.39	0.0024	1206	US-08-911-423-2 x V32773	CC	CC
N_Genesed_34_V41370	+100.50	194.39	0.0024	1206	Align seg 1/1 to: V32773 from: 1 to: 1020	CC	CC
N_Genesed_34_V41370	+100.50	194.39	0.0024	1206	alignment_scores:	CC	CC
N_Genesed_34_V41370	+100.50	194.39	0.0024	1206	Length: 228	CC	CC
N_Genesed_34_V41370	+100.50	194.39	0.0024	1206	Gaps: 0	CC	CC
N_Genesed_34_V41370	+100.50	194.39	0.0024	1206	Percent Identity: 100.000	CC	CC

67 rHisCysGlyAspProGlnCysLysIleCysLysHistYProCysGlnP 84
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 246 CCACCTGTGGAGCCCTCGATCTGCAAGATCTGCAACGACTAACCCCTGCCAAC 295
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 84 roglYglInargvalGluserGlnGlyAspIleValPhedylpheargcys 100
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 296 CAGGCCAACGGTGAGGTCCTCAGGGATATTGTTGGCTTCGGTGT 345
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 101 ValAlaCysAlaIleMetGlyThrPheSerIleGlyArgAspGlyHisCysAr 117
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 346 GrrccCTGRCATGGCACCTTCGAGGNGTAGGTCAGGTCACTGCAG 395
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 117 gLeutItpThrAspCysSerGlnPheGlyPheLeutItpNetPheProGlyA 134
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 396 ACTTGGCCAACGTTCTCAGTTGGATTCTCACCCATGTCCTGGAA 445
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 134 snlysthrHisAsnAlaIaCysIleProGluProLeuProThrGluGln 150
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 446 ACAGAACCCACCATGCTGTCATGCTGCATGCATTTCCT 545
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 151 TyrglyHISLeutItpValIleLeutAlaAlaAlaCysIlePhePhe 167
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 496 TAGGCCAATTGACTGTCACTCTGGCATCTGCATGCATTTCCT 545
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 167 eLeutItpThrValIleLeutIleLeutIleLeutIleLeutIleLeutIle 184
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 596 ACATGTGCTTCAGTCACCTCCAGTTCAGTGTGTCAGTCAGT 645
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 201 GluAspAlaCysSerPheGlnPheProPheAlaGluValIleLeutIle 217
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seq_name: N_Geneseq_34:V19152

seq_documentation_block:

ID V19152 standard; DNA; 1073 BP.

AC W09806842-A1.

PT 19-FEB-1998 (first entry)

KW Nucleotide sequence of the mouse 312C2 T cell gene.

KW Mouse 312C2 T cell protein; thymus cell; spleen cell; T cell; antigen specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoietic cells; lymphoid cell; ss;

KW autoimmune disorders.

OS Mus sp.

FH Location/Qualifiers

FT Key 67 .754

FT CDS /tag= "mouse 312C2 protein"

FT /product= "mouse 312C2 protein"

PN W09806842-A1.

PD 14-AUG-1997; U13931.

PR 07-OCT-1996; US-027901.

PR 16-AUG-1996; US-669443.

PA (SCHERF) SCHEHERZ CORP.

PI Gorman DM, Randall TD, Zlotnik A;

DR WP; 98-15954/14.

DR P-PSDB; W37838.

PT Isolated 312C2 T cell gene used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders

Claim 10; Pages 56-57; 71pp; English.

PT This is the nucleotide sequence encoding the mouse 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement

CC of 312C2 stimulates proliferation of T cell clones, antigen-specific CC proliferation and cytokine production by T-cells, and potentiates T CC cell expansion or apoptosis. The products can be used in the CC treatment of conditions associated with abnormal physiology or CC development, including abnormal proliferation, e.g. cancerous CC conditions or degenerative conditions. They can be used in the CC regulation or development of haematopoietic cells, e.g. lymphoid cells CC which affect immunological responses, e.g. autoimmune disorders. CC Sequence 1073 BP; 243 A; 283 C; 310 G; 237 T;

SO alignment_scores:

Quality: 1195.00	Length: 228
Ratio: 5.241	Gaps: 0
Percent Similarity: 100.000	Percent Identity: 100.000

alignment_block:

US-08-911-423-2 x V19152 .

Align seg 1/1 to: V19152 from: 1 to: 1073

1 MetGlyAlaItpAlaMetLeutItpCysIleValSerMetLeutItpValLeuAla 17
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 68 ATGGGGCAGGGCCATGCGTGTATGGATCTGATGCTGATGCTGCTGGAA 117
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 17 pLeuGlyItpIleProSerValIleGluItpProGlyCysGlyProGlyLysV 34
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 118 CCTAGTCACCCGAGTGTAGTTGAGGCTGGCTGGCCCTGGCAAGG 167
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 34 alGlnAsnGlySerGlyAsnAsnThrArgCysCysSerIleUtyAlaPro 50
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 168 TTCAAACTGGAAACTGTCACAAACTCGTGTGTCACCTGAGTA 217
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 51 GlylysGluaspCysProIlysGluArgCysIleCysValItpProGlyLys 67
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 218 GGCAGGGAGGACTGTCCCAAAGAAAGGTGCATATGTGTCACCTGAGTA 267
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 67 rhiscysGlyAspProGlnCysLysIleCysLysHistYProCysGlnP 84
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 268 CACTGTGGGACCTCTAGGCAAGATCTCAGACTACCCCTGGCAAC 317
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 318 CAGGCCAGGGTGGAGTCAGTCAGGGATATTGTGTTGCTCCGGTGT 367
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 101 ValAlaCysAlaMetGlyItpPheserAlaGlyItpAspGlyHisCysAr 117
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 368 GTTGCTGTGTCCTCCATGGCACCTCTCCGGAGGTGTCAGGTGTCAGTCAGCAG 417
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 117 gLeutItpThrAsnCysSerGlnPheGlyItpLeutItpMetPheProGlyA 134
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 134 snLysThrHisAsnAlaValCysIleProGluProLeuProThrGluGln 150
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 468 ACAAGACCCACAATCTGGCATCCGGCCTACTGCCACTGAGCAA 517
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 151 TyrGlyHisLeutItpValIleLeutIleAlaCysIleLeutIle 167
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 518 TACGSCCATTTGACITGTCATCTTCGGTCATGGCTGCAAGCTTCCT 567
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 167 eLeutItpThrValGlnLeuGlyLeuItpLeuItpArgGlnH 184
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 568 CCTAACCAAGTCGAGCTGGCAATGGAGCTGAGGAGCAAC 617
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 184 isMetCysProArgGluItpGlnProPheAlaGluValGlnLeuSerAla 200
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 618 ACATGTGTCCTCCGAGAACGCCATTCCGGAGCTGGAGCTGTCAGCT 667
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 201 GluaspAlaCysSerPheGlnPheProGlyItpGluArgGlyGluGlnH 217
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 668 GAGGATGCTTGCAGCTTCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 717
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q_name: N_Geneseq_34 :V32774
q_documentation_block:
 V32774 standard; cDNA; 1031 BP.
 V32774;
 29-SEP-1998 (first entry)
 Mouse GITR-B cDNA.
 Mouse glucocorticoid induced TNFR-family related protein; lymphocyte, GITR; tumour necrosis factor; apoptosis; hodgkin's disease; GITR-B; GITR-C; ds.
 Mus sp.
 Key 46 . 930
 CDS
 Location/Qualifiers
 /product= "Mouse GITR-B"
 /tag= q
 /product= "Mouse GITR-B"
 WO9824895-A1.
 11-JUN-1998.
 08-NOV-1997; E06252.
 02-DEC-1998; GB-025074.
 (PHEAA) PARMACIA & UPJOHN SPA.
 Riccardi C;
 WPI; 98-33315/29.
 P-PSDB; WA9017.
 New isolated glucocorticoid induced TNFR related polypeptide - used to stimulate lymphocyte activity and cell death rescue, useful to, e.g. develop products to suppress lymphocyte activity and induce apoptosis.
 Claim 1: Pages 38-40; 53pp; English.
 The present claimed sequence represents a spliced version of the mouse glucocorticoid induced TNFR-family related protein (GTR) cDNA (V32773). The invention also claims for the GITR-C (V22775) cDNA which is another splicing variant of GTR cDNA. The GTRs are claimed to be useful for stimulating lymphocyte activity and cell death rescue. GITR antagonists are claimed to be useful for suppressing the lymphocyte activity and for inducing apoptotic deletion. GTR cDNAs and the proteins they encode are also claimed to be useful for suppressing growth of tumour cells over-expressing GTR or for the treatment of refractory hodgkin's disease. Sequence 1031 BP; 234 A; 272 C; 293 G; 232 T;
alignment_scores:
 Quality: 1161.50 Length: 232
 Ratio: 5.094 Gaps: 2
 Current Similarity: 98.276 Percent Identity: 97.845
alignment_block:
 S-58-911-423-2 x V32774 ..
 11gn seg 1/1 to: V32774 from: 1 to: 1031.
 1 MetGlyAlaTrpAlaMetLeuTyrGlyValSerMetLeuCysValLeuAs 17
 46 ATGGGCCATGGCCATGGCTATGGCTATGGAGTCATCTGTGCTGGA 95
 17 PheGlyGlnProSerAlaValGluIuProGlyGlyProGlyLysV 34
 96 CCTAGTCAGCGAGTGTAGTGAGSGAGCTCTGGCCCTGGCAAGG 145
 34 alginAsnGlySerGlyAsnAsnThrArgCysCysSerLeutYralapro 50
 146 TTCAAGACGGAGTGTCCAAACACTCGCTGAGGCCCTATGGCCA 195
 51 GlyLysGluAspCysProLysGluArgCysIleCysValThrProGlyU 67
 196 GGCAAGCAGGACTGTCAAAAGAAGTCATATGTGTCACACCTGAGTA 245
 67 HisCysGlyAspProGlyCysLysIleCysLysHistYrrCysGlnP 84

the proteins they encode are also claimed to be useful for suppressing growth of tumour cells over-expressing GITR or for the treatment of refractory hodgkin's disease.

Sequence 1087 BP; 246 A; 287 C; 310 G; 244 T; 796 A 796

alignment_scores:

Quality: 1155.00	Length: 251
Ratio: 5.088	Gaps: 2
Percent Similarity: 90.438	Percent Identity: 90.438

alignment_block:

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OS-08-911-423-2 x V32775 ..
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Align seg 1/1 to: V32775 from: 1 to: 1087

1 MetClyAlaItrpAlaMetLeutY GlyVaISeMetIeuCysValLeuAs 17

46 ATGGGGCATGGCCATCTGTAGGAGTCAGTCGAGTCAGTCGTCGTCGA 95

17 pIeuglyGlnProSerValAlaGluGluProGlycSglYProGlyLysV 34

96 CCTAGGTCAGCCAGTGTAGTGGAGGCCCTGGCTGCCCCCTGGCAAGG 145

34 alGlnAsnGlySeGlyAsnAsnThrArgCysSerLeutYalaPro 50

146 TTCTAAACGGAAAGTGGCCACAAACCTCTGGCTGCAGCTGTAGCTCA 195

51 GlyLyGluAspCysProLyGluArgCysSilectysValthrProGlyLu 67

196 GGCAAGGAGGAGCTCCAAAAGGTCATAGTGTCACACTGAGTA 245

67 rHisCysGlyAspProGlnCysLsilectysLsHistYtProCysGlnP 84.

246 CCACTGTGGAGACCTCACTGCAAGATCTGCAACACTAACCCCTGCCAAC 295

84 roGlyGlnArgvalGluSerGlnGlyAspIleValpheGlypheArgCys 100

296 CAGGCCAGGGGGAGCTCAAGGGATATTGTTGCTTCAGCTCGGGT 345

101 ValAlaCysAlaMetGlyThrPheserAlaIgYArgAspGlyHisCysAr 117

346 GTCGCTGTGCCATGGCACCTCTCCGAGGGTGTGACGGTCACTGCGAG 395

117 gLeutThrProAspCysSerGlnInphGlyIleLeutThrMetPheroGlyA 134

396 ACTTGGACCAACTGTTCTCACTGGATTTCACCATGTTCCCTGGGA 445

134 snlysthrHisAsnAlaValCysSileProIuProLeuProThrGluGin 150

446 ACAGRNCCCACAACTGCTGTCATGCCAGCAGCTGCCACTGAGCAA 495

151 TyrglyHisIleuthrVallePhelueValMetAlaAlaCysIlePhPh 167

496 TACGCCCAATTGATGTCACTCTGGTCATGCCTGCATGATTTCTT 545

167 eLeutThrThrValGlnLeuGlyIleAlaHistIleTrpGlnLeuArgGlnH 184

546 CCTAACACAGTCAGTCAGTCGGCCAGCACATGGCAGCTGAGGGCAC 595

184 isMetCysProArg 188

596 ACATGTGCCCCAGGGTCAAGTCAGTGTGTCAGGGAGGGAAAAATGTGTCR 645

189 Glu ThrGlnProheAlaG 195

646 CAGGCCCTCACTTACCGCAGTTTACTACAGAACCCAGCCATCGCGG 695

195 IuvaGlnIleuseFalaGluAspAlaCysSerPhenGlnIleProGluGlu 211

696 AGGRCAGTGTGTCAGCTGAGGATCTGAGTCAGTCCAGTTCCTGAGGGAG 745

212 GluArgGlyGluGluGlnThrGluGluLysCysHisIleuGlyGlyArgTrPr 228

746 GAACGGGGAGCAGACAGAAAAGTGCATCTGGGGGTGGTGGCC 795

228 o 228

796 A 796

seq_name: N_Geneseq_34:v19153

seq_documentation_block:

ID	V19153 standard: DNA; 1006 BP.
AC	V19153;
DT	28-JUL-1998 (first entry)
DE	Nucleotide sequence of the human 312C2 T cell gene.
KW	Human 312C2 T cell protein; thymus cell; spleen cell; T cell; antigen-specific T cell proliferation; cytokine production by T cell; apoptosis; cancer; haematopoietic cells; lymphoid cell; ss; autoimmune disorders.
OS	Homo sapiens.
FH	Key
FT	CDS
FT	1..726
FT	/*tag= a /product= "human 312C2 protein"
FT	PN W09806842-A1.
PD	19-SEP-1998.
PF	14-AUG-1997; U13931.
PR	07-OCT-1996; US-027901.
PR	16-AUG-1996; US-639943.
PA	(SCHIE) SCHERING CORP.
PI	GOITMAN DM, RANDALL TD, ZLOTNIK A;
DR	WPI: 98-15953/14.
DR	P-PDB: W37839.
PT	Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
PT	T cell disorders
PS	Claim 10; Pages 58-59; 71pp; English.
CC	This is the nucleotide sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen specific cell proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
SQ	Sequence 1006 BP; 156 A; 331 C; 337 G; 182 T;

alignment_scores:

Quality:	660.50	Length:	235
Ratio:	3.458	Gaps:	3
Percent Similarity:	81.277	Percent Identity:	57.021

Align seg 1/1 to: V19153 from: 1 to: 1006

1 MetGlyAlaIrrPAlaMetIleutYglyIvalSerMetLeucysvaleuAs 17

19 ATGGGGCGTTTCGGCCCTGGCGCTGCGTCGCGCCCTCAG 68

17 PLeuGlyGluProSerValValGluGluProGlyCysGlyProGlyLysV 34

69 CCTGGCTCACTGCCCT...ACCGGGGGTCCGGGCTGGGCGCC 115

34 alGlnAsnGlySerGlyAsnAsnGlySerGlySerIleutYtala... 49

116 TCCTGCTGGACGGAAACGACGGCTGCTGCGGCTCACRGACG 165

50 ProGlyLysGluAspCysProlysGluAspCysProlysGluArgCys 60

PF 06-MAY-1994; U05036.
 PR 07-MAY-1993; US-0360843.
 PA (IMMV) IMMUNEX CORP.
 PI Alderson MR, Goodwin RG, Smith CA;
 DR WPI: 95-022265/03.
 P-PSDB: R64197.
 DR Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor
 PT 4-1BB to transduce signal
 PS Claim 29; Page 46:47; 65pp; English.
 CC The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see
 CC 075423) are useful in a pharmaceutical composition for stimulating
 CC the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful
 CC for exploring mechanisms of T-cell activation, as they are expressed
 CC on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for
 CC in vitro cultivation of primary T-cells during the derivation of
 CC clonal T-cell lines. It may also be used to stimulate proliferation
 CC of activated T-cells, used in therapeutic procedures. Sequence 1415 BP;
 SQ 385 A; 332 C; 333 G; 365 T;

alignment_scores:
 US-08-911-423-2 x Q75424 .. .
 Align seg 1/1 to: Q75424 from: 1 to: 1415
 Percent Similarity: 49.814

alignment_block:
 US-08-911-423-2 x Q75424 .. .
 Quality: 176.00 Length: 269
 Ratio: 1.313 Gaps: 16
 Percent Identity: 26.022

seq_name: N_Geneseq_34:T91026

seq_documentation_block:
 ID T91026 standard; cDNA to mRNA; 1415 BP.
 AC T91026;
 DT 25-FEB-1998 (first entry)
 DE Human 4-1BB receptor cDNA clone hu4-1BB.
 KW 4-1BB ligand; 4-1BB-L; Receptor; human; cytokine; T lymphocyte;
 KW T cell; proliferation; immunostimulant; ss.
 OS Homo sapiens.
 PH Key Location/Qualifiers
 FT CDS 120..387
 FT /*tag= a
 FT 120..188
 FT /*tag= b
 FT mat_peptide 189..884
 FT /*tag= c
 PN US5674704-A.
 PD 07-OCT-1997.
 PR 07 MAY 1993; 060843.
 PR 06 MAY 1994; US-236918.
 PR 07 MAY 1993; US-060843.
 PA (IMMV) IMMUNEX CORP.
 PI Alderson MR, Goodwin RG, Smith CA;
 DR WPI: 97-502333/46.
 DR P-PSDB: W26658.
 PT DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating
 PT T-cell proliferation in vitro, and as research tools
 PS Example 2; Column 43-44; 32pp; English.
 CC This cDNA clone encodes human 4-1BB (see W26658), a member of the
 CC tumour necrosis factor receptor superfamily that is expressed on
 CC cells that include, but are not limited to, stimulated human
 CC peripheral blood lymphocytes. The clone was isolated from a cDNA
 CC library prepared from human peripheral blood T-lymphocytes that
 CC had been activated with phytohaemagglutinin and phorbol myristate
 CC acetate. A fragment of murine 4-1BB DNA (see T91027) was used
 CC as probe. A novel claimed cytokine, designated 4-1BB ligand
 CC (4-1BB-L), has been identified, cloned and sequenced (see W26657).
 CC that binds to 4-1BB-L, especially its soluble extracellular
 CC domain, can be used to stimulate T-cell proliferation in vitro, as
 CC a research tool and as an affinity ligand for purifying 4-1BB.
 SQ Sequence 1415 BP; 385 A; 332 C; 333 G; 365 T;

alignment_scores:
 Quality: 176.00 Length: 269
 Ratio: 1.313 Gaps: 16
 Percent Similarity: 49.814 Percent Identity: 26.022

seq_name: N_Geneseq_34:T888969

70	YASPPROGLYCYSIIIECYSLYSHISTYRPROCYSGINPROGLYGLNA	87
71	::::: :::: :::: :::: :::: :::: ::::	88
300	GCGGCAGATGGACGACAATGTGAACAG ..GATTGTAACAAACGCTCAAG	346
87	rgValGluSerGlnGlyAspIleValPheGlyPheArgGysValAlaCys	103
347	:::: :::: :::: :::: :::: :::: ::::	104
104	AlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysArgLeuTrpThr	120
111	:::: :::: :::: :::: :::: :::: ::::	111
376	TGCTTGAGAACATTAAACATCAGAAACCTGGCACATCTGACCTGGAC	425
120	rAsnCysSerGlnPheGlyPheLeuThrNetPheProGlyAsnLySThrH	137
426	AACTGTCITTTGGATGGAAAAGCTGTGTGAATGGACGAAGGAGA	475
137	isAsnAlaValCys.	141
476	GGGAGTGGTCCTGGACCATCTAGCCGACCTCTCCGGAGACATCC	525
142	..IleProGluProLeuProThrGluGlnTyrGlyHis.....Le	154
526	TCCTGACCCCCCTGCCGCCCCTGCCGAGAACACTCTCCGAGAT	575
154	uThrValIlePheLeuValAlaAlaCys.....IleP	166
576	CACTCTCTCTCTCTGGCTGACTGGCTGCTCTCTGGCTGT	625
166	hepHeLeuThrThrValGlnIleGlyIleHisIleTrpGlnIleArgArg	182
626	TCCTCTCAG.....CTCGTTCTCTGTGTTAAACCG	660
183	GlnHisMetCysProArgGlu.....	193
661	GGCAGAAAAGAAACTCCCTGTTATATTCAAACACCANT	698
193	eAla...GluValGlnLeuSer...AlaGluAspAlaCysSerPheGlnP	208
699	TATGAGACCATGACAACACTCAAGAGAAAGATGCTAGTCGCGAT	748
208	heProGluGluGluArgGlyGluGlnThrGluGluLysCysHistLeu	223
749	TTCCAGAAAGAAAGA.....GAAGGGGGATGTGAACTG	780
sq_name: N_Geneseq_34:T39546		
sq_documentation_block:		
T39546 standard; cDNA to mRNA; 838 BP.		
T39546;		
12-DEC-1996 (first entry)		
Human receptor H4-1BB CDNA.		
receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte;		
immunomodulant; cancer; autoimmune disease; graft rejection		
therapy; ss.		
Homo sapiens.		
Key		
mat_peptide		
cds		
W09629348-A1.		
26 SEP 1996.		
22-MAR-1996; 003965.		
23-MAR-1995; US-409851.		
(INDV) UNIV INDIANA FOUND.		
Kang C, Kwon BS;		
WPI: 96-43138/44.		
P-PSDBL; WO4174.		
Monoclonal antibody specific for human receptor protein 4-1 to enhance proliferation and activation of T-cells for treating cancer and to inhibit specific ligand binding for treating auto-immune diseases.		

54 spcysPro.....LysGluArgCysIleCysvalThrProGluTyr 67
 |||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 227 TTGGCTCTCACCCAAACGGGAGTGAGTCATT...GAAGGATT 273
 |||:||:||:||:||:||:||:||:||:||:||:||:||:
 68 HisCysGlyAspProGlnCysLysIleCysLysHistidylProCysGlnPr 84
 |||:||:||:||:||:||:||:||:||:||:||:||:||:
 274 CATTGCTGGGCCAACGTGACCAAGATGTGAAAAG...GACTGAGCC 320
 |||:||:||:||:||:||:||:||:||:||:||:
 84 oGlyGinArgValGluSerGlnGlyAspIleValPheGlyPheArgCysV 101
 |||:||:||:||:||:||:||:||:||:||:
 321 TGGCAGGAGCTAACGAGCAGGT...TGCA 349
 |||:||:
 101 alaCysAlaMetGlyThrPheSerAlaGlyArgAsp...GlyHisCys 116
 |||:||:||:||:||:||:||:||:||:
 350 AAACCTGTAGTTGGGACATTATAACCACACGCTACTGGCGrCTGT 399
 |||:||:||:||:||:||:
 117 ArgLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGln 133
 |||:||:||:||:||:||:||:||:||:||:||:
 400 CGACCTGGACGAACTCTCTAGCGGAAGTCAGTGTGCTTAAGACGG 449
 |||:||:||:||:||:||:
 133 yAsnLySthrHisAsnAlaValCys..... 141
 |||:||:||:||:||:
 450 GACCACCGAGAAAGGACCTGGCTGTGGACCCCCCTGTGGTAGCTCTCTC 499
 |||:||:||:||:
 142IleProGluProIleProThrIleGlnItyr 151
 |||:||:||:
 500 CCAGTACCACTATTCTGTAATCTCATAGGGGACAGGGCATTCC 549
 |||:||:||:
 152 GlyHisLeuThrValIlePheLeuValMetAlaAlaCysIlePhePhe... 167
 |||:||:||:
 550 TGCAGGTCCCTAACCTGTTCTGGCTGACATGGCTTTCGGCTGGC 599
 |||:||:
 168LeuThrThrValGlnLeuGlyLeuHistileTrpGlnLeuArgA 182
 |||:||:
 600 CCTGATCTCACTACTCCCTCTCTGTGCTCAATGGATCAGGAAA 649
 |||:||:
 182 rg...GlnHisMetCysProArgGluThrGlnProPheAlaGluValGln 197
 |||:||:
 650 AATTCCCCACATTC.....AGCAACCATTAAAGAGCAACT 690
 |||:||:
 198 LeuSerAla.....GluAspAlaCysSerPheGlnPheProGlnLeuGluG 212
 |||:||:
 691 GGACAGCTCAAGGGAGAATGCTGTAGCTGGCTCACAGGAGAA 740
 |||:||:
 212 uArgGly 214
 |||:
 741 AGAGGA 747
 |||:
 seq_name: N_Geneseq_34:T39541

seq_documentation_block:
 ID T39541 standard; cDNA to mRNA; 2347 BP.
 AC T39541.
 DT 12-DEC-1996 (first entry)
 DE Mouse receptor 4-BB CDNA.
 KW Receptor 4-BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
 KW immunostimulant; cancer; autoimmune disease; graft rejection;
 KW therapy; ss.
 OS Mus sp.
 FH Key
 FQ cds Location/Qualifiers
 FT 146 .916
 FT /*tag a
 FT 146 .913
 FT /*tag= b
 PN W09629348-A1.
 PD 26-SEP-1996.
 DF 22-MAR-1996; 003965.
 PR 23-MAR-1995; US-409851.
 PA (INDV) UNIV INDIANA FOUND.
 PI Kang C., Kwon BS.
 DR WPI; 96-443138/44.
 DR P-PSDB; W04173.

PT Monoclonal antibody specific for human receptor protein 4-1BB - used
 PT to enhance proliferation and activation of T-cells for treatment of
 PT cancer and to inhibit specific ligand binding for treating
 PT auto-immune diseases
 PS Disclosure: Page 32-34; 48pp; English.
 CC A cDNA clone (T39541) codes for novel murine receptor protein
 CC 4-1BB (W04173), a protein that has the potential to function as
 CC an accessory signaling molecule during T-cell activation and
 CC proliferation. The cDNA clone was isolated and identified by
 CC specific expression of T-cell genes. Primers (see also T39542-45)
 CC based on the murine 4-1BB cDNA were utilised in the identification
 CC of the gene (see also T39546) for the human homologue H4-1BB
 CC (W04174), a protein used to raise a monoclonal antibody useful
 CC in cancer and autoimmune disease therapy.
 SQ Sequence 2347 BP; 590 A; 570 C; 580 G; 607 T;

alignment_scores:
 Quality: 153.50 Length: 219
 Ratio: 1.323 Gaps: 11
 Percent Similarity: 52.968 Percent Identity: 27.854
 alignment_block:
 US-08-911-423-2 x T39541 ..
 Align seg 1/1 to: T39541 from: 1 to: 2347
 21 ProSerValIleGluGluProGlyCysGlyProGlyLysValGlnAsnGln 37
 |||:||:||:||:||:
 302 TCCAGGATAGGTGGACAGCGGAAGCTGT 328
 |||:||:||:
 37 ySerGlyAsnAsnThrArgCysSerIleUreaTAlaProGlyLysGluA 54
 |||:||:||:
 329AACATCTGAGGTGGTGAGCTAATTCAGGTCAGAAAGT 371
 |||:||:
 54 spcysPro.....LysGluArgCysIleCysValIthrProGluTyr 67
 |||:||:
 372 TTTCTCCCTACCCACACGCCAGTGTGAGTCATT ..GAAGGATTC 418
 |||:||:
 68 HiscysGlyAspProGlnLysIleCysLysHistidylProCysGlnPr 84
 |||:||:
 419 CATGGCTTGGCCACAGTGACCAAGATGAAAG...GACTGCAGGCC 465
 |||:||:
 84 oGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCysV 101
 |||:||:
 466 TGGCCAGGAGCTAACGAAACAGGGG.....TGA 494
 |||:||:
 101 alaCysAlaMetGlyThrPheserAlaGlyArgAsp...GlyHisCys 116
 |||:||:
 495 AAACCTGAGCTGGAAACATTAAATGACGGAAGGTCTGGCTGTCTG 544
 |||:||:
 117 ArgLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGln 133
 |||:||:
 545 CGACCCCTGGACGAACTGCTCTGTGCTCTAGACGGAAGGTCTGTCTG 594
 |||:||:
 133 yAsnLysThrHisAsnAlaValCys..... 141
 |||:||:
 595 GACCACTGGAAAGGACTGGAAACATTAAATGACGGAAGGTCTGGCTGTCTG 644
 |||:||:
 142IleProGluProLeuProThrGlnGlnItyr 151
 |||:||:
 645 CCAGTACCAACATTCTGTGACTCCAGAGGAGCACGGGGACTCC 694
 |||:||:
 152 GlyHisLeuThrValIleIleLeuValMetAlaAlaCystIlePhePhe.. 167
 |||:||:
 695 TTGAGGGCTCTAACCTGTTCTGGCTGACATGGCTTGTGCTGTGGC 744
 |||:||:
 168LeuThrThrValIleGlyLeuHistileTrpGlnLeuArgA 182
 |||:||:
 745 CCTGATCTCAATTACTCTCTGCTCAATGGATCAGGAAA 794
 |||:||:
 182 rg...GlnHisMetCysProArgGluThrGlnProPheAlaGluValGin 197
 |||:||:

795 AATTCCCCACATTC.....AAGCAACCATTAAAGAAAGACCACT 835
198 LeuSerAla.....GluAspAlaCysSerPheGlnPheProIuGluG1 212
836 GGAGCAGCTCAAGAGGAAGATCCTTGTAAGCTGCCATGTCCACAGGAGA 885
212 uArgGly 214
|
886 AGAGGA 892